

Hanu R Pappu

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

1,239
citations

430874

18
h-index

395702

33
g-index

54
all docs

54
docs citations

54
times ranked

1363
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanotechnology for Plant Disease Management. <i>Agronomy</i> , 2018, 8, 285.	3.0	256
2	Geminiviruses and Plant Hosts: A Closer Examination of the Molecular Arms Race. <i>Viruses</i> , 2017, 9, 256.	3.3	80
3	Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	79
4	Phenotypic and Etiological Differences Between Psyllid Yellows and Zebra Chip Diseases of Potato. <i>American Journal of Potato Research</i> , 2010, 87, 41-49.	0.9	77
5	A novel fungal effector from <i>Puccinia graminis</i> suppressing <i>scp</i> RNA silencing and plant defense responses. <i>New Phytologist</i> , 2019, 222, 1561-1572.	7.3	59
6	Multiplexed editing of a begomovirus genome restricts escape mutant formation and disease development. <i>PLoS ONE</i> , 2019, 14, e0223765.	2.5	50
7	ICTV Virus Taxonomy Profile: Caulimoviridae. <i>Journal of General Virology</i> , 2020, 101, 1025-1026.	2.9	49
8	Use of Electrical Penetration Graph Technology to Examine Transmission of <i>Candidatus Liberibacter solanacearum</i> ™ to Potato by Three Haplotypes of Potato Psyllid (<i>Bactericera cockerelli</i> ; Hemiptera: Tj ETQq0 0 0 BT /Overlock 10 T	0.9	41
9	Evaluation and identification of candidate genes for artificial microRNA-mediated resistance to tomato spotted wilt virus. <i>Virus Research</i> , 2016, 211, 151-158.	2.2	39
10	A new and distinct species in the genus <i>Caulimovirus</i> exists as an endogenous plant pararetroviral sequence in its host, <i>Dahlia variabilis</i> . <i>Virology</i> , 2008, 376, 253-257.	2.4	38
11	Transcriptome-wide identification of host genes targeted by tomato spotted wilt virus-derived small interfering RNAs. <i>Virus Research</i> , 2017, 238, 13-23.	2.2	38
12	Small RNA profiles of wild-type and silencing suppressor-deficient tomato spotted wilt virus infected <i>Nicotiana benthamiana</i> . <i>Virus Research</i> , 2015, 208, 30-38.	2.2	34
13	The Tomato Spotted Wilt Virus Genome Is Processed Differentially in its Plant Host <i>Arachis hypogaea</i> and its Thrips Vector <i>Frankliniella fusca</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1349.	3.6	31
14	In Vivo Localization of Iris yellow spot <i>Tospovirus</i> (Bunyaviridae)-Encoded Proteins and Identification of Interacting Regions of Nucleocapsid and Movement Proteins. <i>PLoS ONE</i> , 2015, 10, e0118973.	2.5	27
15	Comparative analysis of virus-specific small RNA profiles of three biologically distinct strains of Potato virus Y in infected potato (<i>Solanum tuberosum</i>) cv. Russet Burbank. <i>Virus Research</i> , 2014, 191, 153-160.	2.2	23
16	Virus and Viroid-Derived Small RNAs as Modulators of Host Gene Expression: Molecular Insights Into Pathogenesis. <i>Frontiers in Microbiology</i> , 2020, 11, 614231.	3.5	22
17	Movement and nucleocapsid proteins coded by two tospovirus species interact through multiple binding regions in mixed infections. <i>Virology</i> , 2015, 478, 137-147.	2.4	21
18	Comparison of small RNA profiles in <i>Nicotiana benthamiana</i> and <i>Solanum lycopersicum</i> infected by <i>Polygonum ringspot tospovirus</i> reveals host-specific responses to viral infection. <i>Virus Research</i> , 2016, 211, 38-45.	2.2	21

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19	Induction of Plant Resistance in Tobacco (<i>Nicotiana tabacum</i>) against Tomato Spotted Wilt Orthotospovirus through Foliar Application of dsRNA. <i>Viruses</i> , 2021, 13, 662.	3.3	17
20	Current Status and Potential of RNA Interference for the Management of Tomato Spotted Wilt Virus and Thrips Vectors. <i>Pathogens</i> , 2021, 10, 320.	2.8	16
21	The effects of potato virus Y-derived virus small interfering RNAs of three biologically distinct strains on potato (<i>Solanum tuberosum</i>) transcriptome. <i>Virology Journal</i> , 2017, 14, 129.	3.4	15
22	Deriving Economic Models for Pea Aphid (Hemiptera: Aphididae) as a Direct-Pest and a Virus-Vector on Commercial Lentils. <i>Journal of Economic Entomology</i> , 2018, 111, 2225-2232.	1.8	15
23	In silico Prediction and Validations of Domains Involved in <i>Gossypium hirsutum</i> SnRK1 Protein Interaction With Cotton Leaf Curl Multan Betasatellite Encoded Ω C1. <i>Frontiers in Plant Science</i> , 2019, 10, 656.	3.6	15
24	Identification and localization of Tospovirus genus-wide conserved residues in 3D models of the nucleocapsid and the silencing suppressor proteins. <i>Virology Journal</i> , 2019, 16, 7.	3.4	14
25	<i>Iris yellow spot virus</i> on Shallot and Onion in France. <i>Plant Health Progress</i> , 2008, 9, .	1.4	14
26	Increasing Outbreaks and Impact of Iris yellow spot virus in Bulb and Seed Onion Crops in the Imperial and Antelope Valleys of California. <i>Plant Health Progress</i> , 2007, 8, 50.	1.4	10
27	Ω C1, pathogenicity determinant encoded by Cotton leaf curl Multan betasatellite, interacts with calmodulin-like protein 11 (Gh-CML11) in <i>Gossypium hirsutum</i> . <i>PLoS ONE</i> , 2019, 14, e0225876.	2.5	10
28	A loop-mediated isothermal amplification assay for the detection of <i>Dahlia mosaic caulimovirus</i> in <i>Dahlia</i> (<i>Dahlia variabilis</i>). <i>Annals of Applied Biology</i> , 2020, 176, 203-209.	2.5	10
29	Characterization of <i>Iris yellow spot virus</i> from Onion in Arizona. <i>Plant Health Progress</i> , 2008, 9, .	1.4	9
30	Putative Auxin and Light Responsive Promoter Elements From the Tomato spotted wilt tospovirus Genome, When Expressed as cDNA, Are Functional in Arabidopsis. <i>Frontiers in Plant Science</i> , 2019, 10, 804.	3.6	9
31	The Tomato spotted wilt virus (TSWV) Genome is Differentially Targeted in TSWV-Infected Tomato (<i>Solanum lycopersicum</i>) with or without Sw-5 Gene. <i>Viruses</i> , 2020, 12, 363.	3.3	9
32	Identification and Functional Analysis of Four RNA Silencing Suppressors in Begomovirus Croton Yellow Vein Mosaic Virus. <i>Frontiers in Plant Science</i> , 2021, 12, 768800.	3.6	9
33	Global analysis of population structure, spatial and temporal dynamics of genetic diversity, and evolutionary lineages of Iris yellow spot virus (Tospovirus: Bunyaviridae). <i>Gene</i> , 2014, 547, 111-118.	2.2	8
34	Effect of Potato Virus S Infection on Late Blight Resistance in Potato. <i>American Journal of Potato Research</i> , 2014, 91, 642-648.	0.9	8
35	A survey on the infection of Onion yellow dwarf virus and Iris yellow spot tospovirus in seed and bulb productions systems of onion in Calabria, Italy. <i>European Journal of Plant Pathology</i> , 2020, 156, 767-778.	1.7	7
36	Identification and Characterization of Plant-Interacting Targets of Tomato Spotted Wilt Virus Silencing Suppressor. <i>Pathogens</i> , 2021, 10, 27.	2.8	7

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37	Complete Genomic Characterization of Plum bark necrosis stem pitting-associated virus Infecting Sweet Cherry in China. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
38	Sequence characterization, molecular phylogeny reconstruction and recombination analysis of the large RNA of Tomato spotted wilt virus (Tospovirus: Bunyaviridae) from the United States. <i>BMC Research Notes</i> , 2016, 9, 200.	1.4	6
39	Emerging Molecular Links Between Plant Photomorphogenesis and Virus Resistance. <i>Frontiers in Plant Science</i> , 2020, 11, 920.	3.6	6
40	Evaluation of the National Plant Germplasm System's Garlic Collection for Seven Viruses. <i>Plant Health Progress</i> , 2008, 9, .	1.4	5
41	In memoriam " Richard M. Elliott (1954-2015). <i>Journal of General Virology</i> , 2015, 96, 1975-1978.	2.9	4
42	Evaluation of Lisianthus as an Indicator Host for <i>Iris yellow spot virus</i> . <i>Plant Disease</i> , 2011, 95, 1520-1527.	1.4	3
43	Structure and Genome Organization of <i>Cherry Virus A</i> (<i>Capillovirus</i> , <i>Betaflexiviridae</i>) from China Using Small RNA Sequencing. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
44	Whole-Genome Characterization of <i>Prunus necrotic ringspot virus</i> Infecting Sweet Cherry in China. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
45	Complete genome characterization and population dynamics of potato virus Y-NTN strain from India. <i>VirusDisease</i> , 2019, 30, 252-260.	2.0	3
46	Viruses Without Borders: Global Analysis of the Population Structure, Haplotype Distribution, and Evolutionary Pattern of <i>Iris Yellow Spot Orthotospovirus</i> (Family <i>Tospoviridae</i> , Genus) Tj ETQq0 0 0 rgBT /Overlock 1.0 Tf 50 37 Td (Ort	1.0	3
47	Genetic diversity in potato mop-top virus populations in the United States and a global analysis of the PMTV genome. <i>European Journal of Plant Pathology</i> , 2020, 156, 333-342.	1.7	2
48	Susceptibility of <i>Arabidopsis</i> Ecotypes to Infection by <i>Iris yellow spot virus</i> . <i>Plant Health Progress</i> , 2012, 13, .	1.4	2
49	Phylogenetics of tobacco rattle virus isolates from potato (<i>Solanum tuberosum</i> L.) in the USA: a multi-gene approach to evolutionary lineage. <i>Virus Genes</i> , 2022, 58, 42-52.	1.6	2
50	World Society for Virology first international conference: Tackling global virus epidemics. <i>Virology</i> , 2022, 566, 114-121.	2.4	2
51	Dahlia Mosaic-Associated Caulimoviruses in Dahlia in Lithuania. <i>Plant Health Progress</i> , 2009, 10, 49.	1.4	1
52	Genome Sequence of <i>Sclerotinia sclerotiorum</i> Hypovirulence-Associated DNA Virus 1 Found in the Fungus <i>Penicillium olsonii</i> Isolated from Washington State, USA. <i>Microbiology Resource Announcements</i> , 2022, , e0001922.	0.6	1
53	Molecular characterization of the 3' end of <i>Citrus tristeza virus</i> genome from Oman. <i>Indian Phytopathology</i> , 2021, 74, 1147-1150.	1.2	0